WE CLAIM:

1. A method of predicting at least one toxic effect of a compound, comprising:

(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 1-3; wherein differential expression of the genes in Tables 1-3 is indicative of at least one toxic effect.

2. A method of predicting the progression of a toxic effect of a compound, comprising:

(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 1-3; wherein differential expression of the genes in Tables 1-3 is indicative of toxicity progression.

3. A method of predicting the hepatotoxicity of a compound, comprising:

(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 1-3; wherein differential expression of the genes in Tables 1-3 is indicative of hepatotoxicity.

4. A method of identifying an agent that modulates the onset or progression of a toxic response, comprising:

(a) exposing a cell to the agent and a known toxin; and

(b) detecting the expression level of two or more genes from Tables 1-3; wherein differential expression of the genes in Tables 1-3 is indicative of toxicity.

5. A method of predicting the cellular pathways that a compound modulates in a cell, comprising:

(a) detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes from Tables 1-3; wherein differential expression of the genes in Tables 1-3 is associated the modulation of at least one cellular pathway.

6. The method of any one of claims 1-5, wherein the expression levels of at least 3 genes are detected.

7. The method of any one of claims 1-5, wherein the expression levels of at least 4 genes are detected.

8. The method of any one of claims 1-5, wherein the expression levels of at least 5 genes are detected.

9. The method of any one of claims 1-5, wherein the expression levels of at least 6 genes are detected.

10. The method of any one of claims 1-5, wherein the expression levels of at least 7 genes are detected.

11. The method of any one of claims 1-5, wherein the expression levels of at least 8 genes are detected.

12. The method of any one of claims 1-5, wherein the expression levels of at least 9 genes are detected.

13. The method of any one of claims 1-5, wherein the expression levels of at least 10 genes are detected.

14. A method of claim 1 or 2, wherein the effect is selected from the group consisting of hepatitis, liver necrosis, protein adduct formation and fatty liver.

15. A method of claim 3, wherein the hepatotoxicity is associated with at least one liver disease pathology selected from the group consisting of hepatitis, liver necrosis, protein adduct formation and fatty liver.

16. A method of claim 5, wherein the cellular pathway is modulated by a toxin selected from the group consisting of amitryptiline, ANIT, acetaminophen, carbon tetrachloride, cyproterone acetate, diclofenac, estradiol, indomethacin, valproate, and WY-14643.

17. A set of at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 1-3.

18. A set of probes according to claim 17, wherein the set comprises probes that hybridize to at least 3 genes.

19. A set of probes according to claim 17, wherein the set comprises probes that hybridize to at least 5 genes.

20. A set of probes according to claim 17, wherein the set comprises probes that hybridize to at least 7 genes.

21. A set of probes according to claim 17, wherein the set comprises probes that hybridize to at least 10 genes.

22. A set of probes according to any one of claims 17-21, wherein the probes are attached to a solid support.

23. A set of probes according to claim 22, wherein the solid support is selected from the group consisting of a membrane, a glass support and a silicon support.

24. A solid support comprising at least two probes, wherein each of the probes comprises a sequence that specifically hybridizes to a gene in Tables 1-3.

25. A solid support of claim 24, wherein the solid support is an array comprising at least 10 different oligonucleotides in discrete locations per square centimeter.

26. A solid support of claim 25, wherein the array comprises at least 100 different oligonucleotides in discrete locations per square centimeter.

27. A solid support of claim 25, wherein the array comprises at least 1000 different oligonucleotides in discrete locations per square centimeter.

28. A solid support of claim 25, wherein the array comprises at least 10,000 different oligonucleotides in discrete locations per square centimeter.

29. A computer system comprising:

(a) a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes in Tables 1-3; and

(b) a user interface to view the information.

30. A computer system of claim 29, wherein the database further comprises sequence information for the genes.

31. A computer system of claim 29, wherein the database further comprises information identifying the expression level for the set of genes in the tissue or cell sample before exposure to a hepatotoxin.

32. A computer system of claim 29, wherein the database further comprises information identifying the expression level of the set of genes in a tissue or cell sample exposed to at least a second hepatotoxin.

33. A computer system of any of claims 29-32, further comprising records including descriptive information from an external database, which information correlates said genes to records in the external database.

34. A computer system of claim 33, wherein the external database is GenBank.

35. A method of using a computer system of any one of claims 29-32 to present information identifying the expression level in a tissue or cell of at least one gene in Tables 1-3, comprising:

(a) comparing the expression level of at least one gene in Tables 1-3 in a tissue or cell exposed to a test agent to the level of expression of the gene in the database.

36. A method of claim 35, wherein the expression levels of at least two genes are compared.

37. A method of claim 35, wherein the expression levels of at least five genes are compared.

38. A method of claim 35, wherein the expression levels of at least ten genes are compared.

39. A method of claim 35, further comprising the step of displaying the level of expression of at least one gene in the tissue or cell sample compared to the expression level when exposed to a toxin.

40. A method of claim 4, wherein the known toxin is a hepatotoxin.

41. A method of claim 37, wherein the hepatotoxin is selected from the group consisting of ANIT, acetaminophen, carbon tetrachloride, cyproterone acetate, diclofenac, estradiol, indomethacin, valproate, and WY-14643.

42. A method of any one of claims 1-5, wherein nearly all of the genes in Tables 1-3 are detected.

43. A method of claim 42, wherein all of the genes in any one of Tables 3A-3S are detected.

44. A kit comprising at least one solid support of any one of claims 24-28 packaged with gene expression information for said genes.

45. A kit of claim 44, wherein the gene expression information comprises gene expression levels in a tissue or cell sample exposed to a hepatotoxin.

46. A kit of claim 45, wherein the gene expression information is in an electronic format.

47. A method of any one of claims 1-5, wherein the compound exposure is *in vivo* or *in vitro*.

48. A method of any one of claims 1-5, wherein the level of expression is detected by an amplification or hybridization assay.

49. A method of claim 48, wherein the amplification assay is quantitative or semi-quantitative PCR.

50 A method of claim 48, wherein the hybridization assay is selected from the group consisting of Northern blot, dot or slot blot, nuclease protection and microarray assays.

51. A method of identifying an agent that modulates at least one activity of a protein encoded by a gene in Tables 1-3 comprising:

(a) exposing the protein to the agent; and

(b) assaying at least one activity of said protein.

52. A method of claim 51 wherein the agent is exposed to a cell expressing the protein.

53. A method of claim 52 wherein the cell is exposed to a known toxin.

54. A method of claim 53 wherein the toxin modulates the expression of the protein.

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